

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (currently amended) A system comprising
an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that comprises a first protein binding site and a second protein binding site, where said first and second protein binding sites specifically bind the same nucleic acid binding protein, and where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a the nucleic acid binding protein, said second binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a the nucleic acid binding protein, said first binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said first binding site; and

a the nucleic acid binding protein that specifically binds said first protein binding site or said second protein binding site.

2. (previously amended) The system of claim 1, wherein said nucleic acid is a double-stranded nucleic acid.

3. (previously amended) The system of claim 1, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

4. (previously amended) The system of claim 1, wherein said first binding site and said second binding site have the same nucleotide sequence.

5. (previously amended) The system of claim 1, wherein said first binding site and said second binding site have the nucleotide sequence of SEQ ID NO: 1.

6. (currently amended) The system of claim 1, wherein said ~~first binding site or said second binding site is specifically recognized and bound by a~~ nucleic acid binding protein is selected from the group consisting of Fis, and Tus.

7. (currently amended) The system of claim 1, wherein said ~~first binding site or said second binding site is bound by~~ nucleic acid binding protein is EF-tu.

8. (previously amended) The system of claim 1, wherein said first binding site is within 20 nucleotides of said second binding site.

9. (previously amended) The system of claim 1, wherein said first binding site is within 11 nucleotides of said second binding site.

10. (previously amended) The system of claim 8, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

11. (previously amended) The system of claim 1, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

12. (withdrawn, non-elected species) The composition of claim 1, further comprising a third protein binding site wherein said third site is in proximity to said first protein binding site or to said second protein binding site such that specific binding of said third binding site with a protein precludes specific protein binding of said first or said second protein binding sites.

13. (previously amended) The system of claim 1, wherein:
said first protein binding site is a Fis binding site;
said second protein binding site is a Fis binding site; and
said binding sites are separated from each other by less than 12 nucleotide base pairs.
14. (previously amended) The system of claim 13, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.
15. (withdrawn, non-elected species) A composition comprising, an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that comprises a first protein binding site, a second protein binding site, and a third protein binding site where said protein binding sites are spaced in proximity to each other such that:
when either said first protein binding site or said third protein binding is specifically bound by a nucleic acid binding protein, said second binding site cannot be bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said second binding site; and
where said first protein binding site and said third protein binding site can simultaneously be specifically bound by a nucleic acid binding protein.
16. (withdrawn, non-elected species) The composition of claim 15, wherein said first protein binding site or said third protein binding site is bound by a nucleic acid binding protein.
17. (withdrawn, non-elected species) The composition of claim 15, wherein said third protein binding site is bound by a nucleic acid binding protein.
18. (withdrawn, non-elected species) The composition of claim 17, wherein said binding protein is attached to a gene transactivator.

19. (withdrawn, non-elected species) The composition of claim 18, wherein said transactivator is a Gal4 transactivator.

20. (withdrawn, non-elected species) The composition of claim 15, further comprising a gene or cDNA under the control of said transactivator.

21. (withdrawn, non-elected species) The composition of claim 20, further comprising a gene or cDNA under the control of said transactivator.

22. (withdrawn, non-elected species) The composition of claim 21, wherein said gene is a reporter gene.

23. (withdrawn, non-elected species) The composition of claim 21, wherein said gene encodes a nucleic acid binding protein.

24. (withdrawn, non-elected species) The composition of claim 15, wherein said nucleic acid is a double-stranded nucleic acid.

25. (withdrawn, non-elected species) The composition of claim 15, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

26. (withdrawn, non-elected species) The composition of claim 15, wherein said first binding site and said third binding site have the same nucleotide sequence.

27. (withdrawn, non-elected species) The composition of claim 15, wherein said first binding site or said second binding Site is specifically recognized and bound by a protein selected from the group consisting of Fis, and Tus.

28. (withdrawn, non-elected species) The composition of claim 15, wherein said first binding site or said second binding site is bound by EF-tu.

29. (withdrawn, non-elected species) The composition of claim 15, wherein said first binding site is within 20 nucleotides of said second binding site.

30. (withdrawn, non-elected species) The composition of claim 15, wherein said first binding site is within 11 nucleotides of said second binding site.

31. (withdrawn, non-elected species) The composition of claim 30, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

32. (withdrawn, non-elected species) The composition of claim 15, wherein the difference in strength between said first protein binding site and said second protein binding site is at least 0 bits as determined by individual information theory.

33. (withdrawn, non-elected species) The composition of claim 1, wherein:
said first protein binding site is a Fis binding site;
said third protein binding site is a Fis binding site.

34. (currently amended) A composition for the storage of binary information, said composition comprising an isolated nucleic acid having a length of at least 3 base pairs and having a nucleotide sequence that encodes a first protein binding site and a second protein binding site, where said first and second protein binding sites specifically bind the same nucleic acid binding protein, and where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by the a protein, said second binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a the protein, said first binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said first binding site; and

further comprising the a nucleic acid binding protein bound to said ~~said~~ first protein binding site or said second protein binding site.

35. (original) The composition of claim 34, wherein said nucleic acid is a double-stranded nucleic acid.

36. (original) The composition of claim 34, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

37. (original) The composition of claim 34, wherein said first binding site and said second binding site have the same nucleotide sequence.

38. (currently amended) The composition of claim 34, wherein said ~~first binding site or said second binding site is specifically recognized and bound by a~~ nucleic acid binding protein is selected from the group consisting of Fis, and Tus.

39. (original) The composition of claim 34, wherein said first binding site is within 20 nucleotides of said second binding site.

40. (currently amended) The composition of claim 34, wherein said first binding site is within ~~20~~ 11 nucleotides of said second binding site.

41. (original) The composition of claim 40, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

42. (previously amended) The composition of claim 34, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

43. (withdrawn, non-elected species) The composition of claim 34, further comprising a third protein binding site wherein said third site is in proximity said first protein binding site or said second protein binding site such that specific binding of said third binding

site with a protein precludes specific protein binding of said first or said second protein binding sites.

44. (original) The composition of claim 34, wherein:
said first protein binding site is a Fis binding site;
said second protein binding site is a Fis binding site;
and said binding sites are separated from each other by less than 12 nucleotide base pairs.

45. (original) The composition of claim 44, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

46. (original) The composition of claim 34, wherein said binding protein is attached to a gene transactivator.

47. (original) The composition of claim 46, wherein said transactivator is a Gal4 transactivator.

48. (original) The composition of claim 46, further comprising a gene or cDNA under the control of said transactivator.

49. (original) The composition of claim 48, wherein said gene is a reporter gene.

50. (original) The composition of claim 48, wherein said gene encodes a nucleic acid binding protein.

51. (currently amended) A method of storing information, said method comprising the step of:

binding a nucleic acid binding protein to a first protein binding site on a nucleic acid, wherein said nucleic acid has a length of at least 3 base pairs and said nucleic acid comprises [encodes] said first protein binding site and a second protein binding site, where said first and second protein binding sites specifically bind the same nucleic acid binding protein, and where said first and second protein binding sites are spaced in proximity to each other such that:

when said first protein binding site is specifically bound by a the protein, said second binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said second binding site; and

when said second binding site is specifically bound by a the protein, said first binding site cannot be bound by a second molecule of the protein that otherwise specifically recognizes and binds said first binding site.

52. (original) The method of claim 51, further comprising the step of determining which binding site on said nucleic acid is bound by said binding protein.

53. (original) The method of claim 51, wherein said nucleic acid is a double-stranded nucleic acid.

54. (original) The method of claim 51, wherein said nucleic acid is a deoxyribonucleic acid (DNA).

55. (original) The method of claim 51, wherein said first binding site and said second binding site have the same nucleotide sequence.

56. (original) The method of claim 55, wherein said first binding site and said second binding site have the nucleotide sequence of SEQ ID NO: 1.

57. (currently amended) The method of claim 51, wherein said first binding site or said second binding site is specifically recognized and bound by a nucleic acid binding protein selected from the group consisting of Fis, EF-tu, and Tus.

58. (original) The method of claim 51, wherein said first binding site is within 20 nucleotides of said second binding site.

59. (original) The method of claim 51, wherein said first binding site is within 11 nucleotides of said second binding site.

60. (original) The method of claim 51, wherein said first binding site has a strength of at least 2.4 bits as determined by individual information theory.

61. (previously amended) The method of claim 51, wherein there is a difference in strength between said first protein binding site and said second protein binding site of more than 0 bits as determined by individual information theory.

62. (original) The method of claim 51, wherein:
said first protein binding site is a Fis binding site;
said second protein binding site is a Fis binding site; and
said binding sites are separated from each other by less than 12 nucleotide base pairs.

63. (previously amended) The system of claim 13, wherein said nucleic acid is a deoxyribonucleic acid comprising the sequence of SEQ ID NO: 2 or SEQ ID NO: 3.

64. (withdrawn, non-elected species) A method of transforming binary information, said method comprising the steps of:

(i) binding a nucleic acid binding protein to an input protein binding site on a first nucleic acid; and

(ii) determining whether or not a nucleic acid binding protein can bind to an output protein binding site on a second nucleic acid;

wherein said first nucleic acid is an isolated nucleic acid having a length of at least 5 base pairs and having a nucleotide sequence that encodes a first protein binding site, a second protein binding site, and a third protein binding site where said protein binding sites are spaced in proximity to each other such that:

when either said first protein binding site or said third protein binding is specifically bound by a nucleic acid binding protein, said second binding site cannot be bound by a nucleic acid binding protein that otherwise specifically recognizes and binds said second binding site; and

where said first protein binding site and said third protein binding site can simultaneously be specifically bound by a nucleic acid binding protein.

65. (withdrawn, non-elected species) The method of claim 64, wherein said first nucleic acid and said second nucleic acid are the same nucleic acid.